

Amendments to the Claims

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

Claims 1-14 (canceled)

Claim 15 (currently amended) A method for assembling sequence reads, comprising the steps of:

- a) providing a plurality of sequence reads into a computer;
- ~~a)~~ b) categorizing within the computer, [[a]] the plurality of sequence reads into at least two sub-groups of sequence reads based on an identifiable characteristic of the sequence reads in each sub-group;
- ~~b)~~ c) matching sequence[[s]] reads within each sub-group thereby creating assemblies of said sequence reads within each respective sub-group; and
- ~~e)~~ d) repeating steps ~~a~~ b) and ~~b~~ c) with all unassembled sequence reads and newly created assemblies; and
- e) providing an assembled sequence to a user.

Claim 16 (original) A method as set forth in claim 15, wherein said categorizing step includes identifying sequence reads having similar sizes.

Claim 17 (withdrawn) A method as set forth in claim 15, wherein said categorizing step includes identifying sequence reads having similar entropies.

Claim 18 (withdrawn) A method as set forth in claim 15, wherein said categorizing step includes identifying sequence reads having similar GC percentages.

Claim 19 (withdrawn) A method as set forth in claim 15, wherein said categorizing step includes identifying sequence reads having similar longest repeats.

Claim 20 (withdrawn) A method as set forth in claim 15, wherein said categorizing step includes identifying sequence reads having similar natures of regions of high entropy.

Claim 21 (withdrawn) A method as set forth in claim 15, wherein said categorizing step includes identifying sequence reads having similar natures of regions of low entropy.

Claim 22 (withdrawn) A method as set forth in claim 15, wherein said categorizing step includes identifying sequence reads having similar compression ratios.

Claim 23 (withdrawn) A method as set forth in claim 15, wherein said categorizing

step includes identifying sequence reads having compression ratios after sequence appending.

Claim 24 (withdrawn) A method as set forth in claim 15, wherein said categorizing step includes identifying sequence reads having two or more similar characteristics.

Claim 25 (currently amended) A method as set forth in claim 15, wherein said categorizing step includes identifying sequence reads having at least one of the following similar identifiable characteristics: sizes, entropies, GC (guanine cytosine) percentages, longest repeats, natures of regions of high entropy, natures of regions of low entropy, and compression ratios.

Claim 26 (currently amended) A method as set forth in claim 25, further comprising a step d) that comprises repeating steps a) b) and b) c) with an identifiable characteristic different from the identifiable characteristic used in step e) b).

Claim 27 (new) A method as set forth in claim 15, wherein matching step comprises using PHRAP (phragment assembly program).